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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/759,803

DATE: 09/17/2004

TIME: 09:07:36

Input Set : N:\CrF3\RULE60\10759803.raw.txt
 Output Set: N:\CRF4\09172004\J759803.raw

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1 <110> APPLICANT: AFAR, Daniel E. H.
2   HUBERT, Rene S.
3   LEONG, Kahan
4   RAITANO, Arthur B.
5   SAFFRAN, Douglas C.
6 <120> TITLE OF INVENTION: NOVEL PROSTATE-RESTRICTED GENE EXPRESSED
7   IN PROSTATE CANCER
8 <130> FILE REFERENCE: 129.13USU1
9 <140> CURRENT APPLICATION NUMBER: US/10/759,803
10 <141> CURRENT FILING DATE: 2004-01-16
11 <150> PRIOR APPLICATION NUMBER: US/09/547,788
12 <151> PRIOR FILING DATE: 2000-04-12
14 <150> PRIOR APPLICATION NUMBER: US 60/128,860
15 <151> PRIOR FILING DATE: 1999-04-12
16 <160> NUMBER OF SEQ ID NOS: 30
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 3051
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapien
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (163)...(1365)
26 <400> SEQUENCE: 1
27      gacgcgtggg cgccggaggcg ctggggcgcac ggccgcggagc cggccggagc tcgaggccgg      60
28      cggcggcggg agagcgaccc gggccgcctc gtacgggggc cccggatccc cgagtggcgg      120
29      ccggagcctc gaaaagagat tctcagcgct gattttgaga tg atg ggc ttg gga      174
30                                         Met Gly Leu Gly
31                                         1
32      aac ggg cgt cgc agc atg aag tcg ccg ccc ctc gtg ctg gcc gcc ctg      222
33      Asn Gly Arg Arg Ser Met Lys Ser Pro Pro Leu Val Leu Ala Ala Leu
34      5          10           15           20
35      gtg gcc tgc atc atc gtc ttg ggc ttc aac tac tgg att gcg agc tcc      270
36      Val Ala Cys Ile Ile Val Leu Gly Phe Asn Tyr Trp Ile Ala Ser Ser
37      25          30           35
38      cgg agc gtg gac ctc cag aca cgg atc atg gag ctg gaa ggc agg gtc      318
39      Arg Ser Val Asp Leu Gln Thr Arg Ile Met Glu Leu Glu Gly Arg Val
40      40          45           50
41      cgc agg gcg gct gca gag aga ggc gcc gtg gag ctg aag aag aac gag      366
42      Arg Arg Ala Ala Ala Glu Arg Gly Ala Val Glu Leu Lys Lys Asn Glu
43      55          60           65
44      ttc cag gga gag ctg gag aag cag cgg gag cag ctt gac aaa atc cag      414
45      Phe Gln Gly Leu Glu Lys Gln Arg Glu Gln Leu Asp Lys Ile Gln

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46	70	75	80	
47	tcc agc cac aac ttc cag ctg gag agc gtc aac aag ctg tac cag gac			462
48	Ser Ser His Asn Phe Gln Leu Glu Ser Val Asn Lys Leu Tyr Gln Asp			
49	85 90 95 100			
50	gaa aag gcg gtt ttg gtg aat aac atc acc aca ggt gag agg ctc atc			510
51	Glu Lys Ala Val Leu Val Asn Asn Ile Thr Thr Gly Glu Arg Leu Ile			
52	105 110 115			
53	cga gtg ctg caa gac cag tta aag acc ctg cag agg aat tac ggc agg			558
54	Arg Val Leu Gln Asp Gln Leu Lys Thr Leu Gln Arg Asn Tyr Gly Arg			
55	120 125 130			
56	ctg cag cag gat gtc ctc cag ttt cag aag aac cag acc aac ctg gag			606
57	Leu Gln Gln Asp Val Leu Gln Phe Gln Lys Asn Gln Thr Asn Leu Glu			
58	135 140 145			
59	agg aag ttc tcc tac gac ctg agc cag tgc atc aat cag atg aag gag			654
60	Arg Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn Gln Met Lys Glu			
61	150 155 160			
62	gtg aag gaa cag tgt gag gag cga ata gaa gag gtc acc aaa aag ggg			702
63	Val Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val Thr Lys Lys Gly			
64	165 170 175 180			
65	aat gaa gct gta gct tcc aga gac ctg agt gaa aac aac gac cag aga			750
66	Asn Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp Gln Arg			
67	185 190 195			
68	cag cag ctc caa gcc ctc agt gag cct cag ccc agg ctg cag gca gca			798
69	Gln Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg Leu Gln Ala Ala			
70	200 205 210			
71	ggc ctg cca cac aca gag gtg cca caa ggg aag gga aac gtg ctt ggt			846
72	Gly Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly Asn Val Leu Gly			
73	215 220 225			
74	aac agc aag tcc cag aca cca gcc ccc agt tcc gaa gtg gtt ttg gat			894
75	Asn Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser Glu Val Val Leu Asp			
76	230 235 240			
77	tca aag aga caa gtt gag aaa gag gaa acc aat gag atc cag gtg gtg			942
78	Ser Lys Arg Gln Val Glu Lys Glu Glu Thr Asn Glu Ile Gln Val Val			
79	245 250 255 260			
80	aat gag gag cct cag agg gac agg ctg ccg cag gag cca ggc cgg gag			990
81	Asn Glu Glu Pro Gln Arg Asp Arg Leu Pro Gln Glu Pro Gly Arg Glu			
82	265 270 275			
83	cag gtg gtg gaa gac aga cct gta ggt gga aga ggc ttc ggg gga gcc			1038
84	Gln Val Val Glu Asp Arg Pro Val Gly Gly Arg Gly Phe Gly Gly Ala			
85	280 285 290			
86	gga gaa ctg ggc cag acc cca cag gtg cag gct gcc ctg tca gtg agc			1086
87	Gly Glu Leu Gly Gln Thr Pro Gln Val Gln Ala Ala Leu Ser Val Ser			
88	295 300 305			
89	cag gaa aat cca gag atg gag ggc cct gag cga gac cag ctt gtc atc			1134
90	Gln Glu Asn Pro Glu Met Glu Gly Pro Glu Arg Asp Gln Leu Val Ile			
91	310 315 320			
92	ccc gac gga cag gag gag cag gaa gct gcc ggg gaa ggg aga aac			1182
93	Pro Asp Gly Gln Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn			
94	325 330 335 340			

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95	cag cag aaa ctg aga gga gaa gat gac tac aac atg gat gaa aat gaa	1230
96	Gln Gln Lys Leu Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu	
97	345 350 355	
98	gca gaa tct gag aca gac aag caa gca gcc ctg gca ggg aat gac aga	1278
99	Ala Glu Ser Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg	
100	360 365 370	
101	aac ata gat gtt ttt aat gtt gaa gat cag aaa aga gac acc ata aat	1326
102	Asn Ile Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn	
103	375 380 385	
104	tta ctt gat cag cgt gaa aag cgg aat cat aca ctc tga attgaactgg	1375
105	Leu Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu *	
106	390 395 400	
107	aatcacatat ttcacaacag ggccgaagag atgactataa aatgttcatg agggactgaa	1435
108	tactgaaaac tgtgaaatgt actaaataaa atgtacatct gaagatgatt atttgtgaaat	1495
109	tttagtatgc actttgtgta gaaaaaaatg gaatggctt taaaacagct tttggggggt	1555
110	actttggaaatg tgtctaataa ggtgtcacaa ttttggttag tagtatttc gtgagaagtt	1615
111	caacacccaa actggaacat agttctcctt caagtgttgg cgacagcggg gcttcctgat	1675
112	tctggaatat aactttgtgt aaattaacag ccacctatacg aagagtccat ctgctgtgaa	1735
113	ggagagacag agaactctgg gttccgtcgt cctgtccacg tgctgtacca agtgcgtgg	1795
114	ccagcctgtt acctgttctc actgaaaagt ctggctaatg ctcttgcgt gtcacttctg	1855
115	attctgacaa tcaatcaatc aatggccctag agcactgact gttAACACAA acgtcactag	1915
116	caaAGTAGCA acagctttaa gtctaaatac aaagctgttc tgtgtgagaa tttttaaaaa	1975
117	ggctacttgt ataataaccc ttgtcatttt taatgtacaa aacgctatta agtggcttag	2035
118	aatttgaaca tttgtgtct ttatTTTCT tgcttcgtgt gtggcaaaag caacatctc	2095
119	cctaaatata tattaccaag aaaAGCAAGA agcagattag gttttgaca aaACAAACAG	2155
120	gccAAAAGGG ggctgacctg gaggcagagca tggtagaggg caaggcatga gagggcaagt	2215
121	ttgttgtgaa cagatctgt cctactttat tactggagta aaagaaaaaca aagttcattg	2275
122	atgtcgaagg atataatacg tggtagaaat taggactgtt tagaaaaaaca ggaataacaat	2335
123	ggttgtttt atcatagtgt acacatttag cttgtggtaa atgactcaca aaactgattt	2395
124	taaaatcaag ttaatgtgaa ttttggaaat tactacttaa tcctaattca caataacaat	2455
125	ggcattaagg tttgacttga gttggctt agtattattt atggtaaataa ggcttacc	2515
126	acttgcAAAT aactggccac atcattaatg actgacttcc cagtaaggct ctctaaagggg	2575
127	taagtaggag gatccacagg atttgagatg ctaaggcccc agagatcggt tgatccaacc	2635
128	ctcttatttt cagaggggaa aatggggccct agaagttaca gagcatctag ctggcgcgt	2695
129	ggcacccctg gcctcacaca gactcccggag tagctggac tacaggcaca cagtcactga	2755
130	agcaggccct gtttgcatt cacgttgcctt cctccaaactt aaacatttt catatgtgat	2815
131	gtccttagtc actaaggta aactttccca cccagaaaaag gcaacttaga taaaatctta	2875
132	gagtacttca atactttct aagtccctt ccagcctcac tttgagtctt cttgggggtt	2935
133	gataggaatt ttctcttgc ttctcaataa agtctctt catctcatgt ttaatttgta	2995
134	cgcatagaat tgctgagaaa taaaatgttc tgttcaactt aaaaaaaaaaaaaaa	3051
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137	<211> LENGTH: 400	
138	<212> TYPE: PRT	
139	<213> ORGANISM: Homo sapien	
140	<220> FEATURE:	
141	<221> NAME/KEY: SIGNAL	
142	<222> LOCATION: (1)...(29)	
143	<400> SEQUENCE: 2	
144	Met Gly Leu Gly Asn Gly Arg Arg Ser Met Lys Ser Pro Pro Leu Val	

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145	1	5	10	15
146	Leu Ala Ala Leu Val Ala Cys Ile Ile Val Leu Gly Phe Asn Tyr Trp			
147	20	25	30	
148	Ile Ala Ser Ser Arg Ser Val Asp Leu Gln Thr Arg Ile Met Glu Leu			
149	35	40	45	
150	Glu Gly Arg Val Arg Arg Ala Ala Ala Glu Arg Gly Ala Val Glu Leu			
151	50	55	60	
152	Lys Lys Asn Glu Phe Gln Gly Glu Leu Glu Lys Gln Arg Glu Gln Leu			
153	65	70	75	80
154	Asp Lys Ile Gln Ser Ser His Asn Phe Gln Leu Glu Ser Val Asn Lys			
155	85	90	95	
156	Leu Tyr Gln Asp Glu Lys Ala Val Leu Val Asn Asn Ile Thr Thr Gly			
157	100	105	110	
158	Glu Arg Leu Ile Arg Val Leu Gln Asp Gln Leu Lys Thr Leu Gln Arg			
159	115	120	125	
160	Asn Tyr Gly Arg Leu Gln Gln Asp Val Leu Gln Phe Gln Lys Asn Gln			
161	130	135	140	
162	Thr Asn Leu Glu Arg Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn			
163	145	150	155	160
164	Gln Met Lys Glu Val Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val			
165	165	170	175	
166	Thr Lys Lys Gly Asn Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn			
167	180	185	190	
168	Asn Asp Gln Arg Gln Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg			
169	195	200	205	
170	Leu Gln Ala Ala Gly Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly			
171	210	215	220	
172	Asn Val Leu Gly Asn Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser Glu			
173	225	230	235	240
174	Val Val Leu Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr Asn Glu			
175	245	250	255	
176	Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu Pro Gln Glu			
177	260	265	270	
178	Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val Gly Gly Arg Gly			
179	275	280	285	
180	Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro Gln Val Gln Ala Ala			
181	290	295	300	
182	Leu Ser Val Ser Gln Glu Asn Pro Glu Met Glu Gly Pro Glu Arg Asp			
183	305	310	315	320
184	Gln Leu Val Ile Pro Asp Gly Gln Glu Glu Glu Gln Glu Ala Ala Gly			
185	325	330	335	
186	Glu Gly Arg Asn Gln Gln Lys Leu Arg Gly Glu Asp Asp Tyr Asn Met			
187	340	345	350	
188	Asp Glu Asn Glu Ala Glu Ser Glu Thr Asp Lys Gln Ala Ala Leu Ala			
189	355	360	365	
190	Gly Asn Asp Arg Asn Ile Asp Val Phe Asn Val Glu Asp Gln Lys Arg			
191	370	375	380	
192	Asp Thr Ile Asn Leu Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu			
193	385	390	395	400

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195 <210> SEQ ID NO: 3
196 <211> LENGTH: 4
197 <212> TYPE: PRT
198 <213> ORGANISM: Homo sapien
199 <400> SEQUENCE: 3
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201 1
203 <210> SEQ ID NO: 4
204 <211> LENGTH: 4
205 <212> TYPE: PRT
206 <213> ORGANISM: Homo sapien
207 <400> SEQUENCE: 4
208 Asn Gln Thr Asn
209 1
211 <210> SEQ ID NO: 5
212 <211> LENGTH: 4
213 <212> TYPE: PRT
214 <213> ORGANISM: Homo sapien
215 <400> SEQUENCE: 5
216 Asn His Thr Leu
217 1
219 <210> SEQ ID NO: 6
220 <211> LENGTH: 4
221 <212> TYPE: PRT
222 <213> ORGANISM: Homo sapien
223 <400> SEQUENCE: 6
224 Arg Lys Phe Ser
225 1
227 <210> SEQ ID NO: 7
228 <211> LENGTH: 4
229 <212> TYPE: PRT
230 <213> ORGANISM: Homo sapien
231 <400> SEQUENCE: 7
232 Lys Arg Asp Thr
233 1
235 <210> SEQ ID NO: 8
236 <211> LENGTH: 4
237 <212> TYPE: PRT
238 <213> ORGANISM: Homo sapien
239 <400> SEQUENCE: 8
240 Thr Thr Gly Glu
241 1
243 <210> SEQ ID NO: 9
244 <211> LENGTH: 4
245 <212> TYPE: PRT
246 <213> ORGANISM: Homo sapien
247 <400> SEQUENCE: 9
248 Thr Asn Leu Glu
249 1

VERIFICATION SUMMARY

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